SPECIFICATION

ALPHA 1-6 FUCOSYLTRANSFERASE

Technical Field

The present invention relates to an α1-6 fucosyltransferase derived from pig or human. More particularly, the present invention relates to a novel α1-6 fucosyltransferase derived from human, which is an enzyme that transfers fucose from guanosine diphosphate (GDP)-fucose by α1→6 linkage to N-acetylglucosamine (GlcNAc) bound to Asn at the stem of asparagine type sugar chain (Asn type sugar chain) and which is useful in the field of glyco-technology for modification and synthesis of sugar chain and/or for the diagnosis of diseases such as malignant tumor, and to a gene encoding said enzyme.

Background Art

The structure and function of sugar chain moiety of complex carbohydrates, such as glycoprotein and glycolipid, derived from higher organisms have been drawing much attention in recent years, and many studies are under way. While a sugar chain is formed by the action of glycohydrolase and glycosyltransferase, glycosyltransferase contributes greatly to its formation.

Using a sugar nucleotide as a sugar donor, glycosyltransferase transfers a sugar to a receptor sugar chain, thereby to elongate the sugar chain. The specificity for the structure of receptor sugar chain is stringent, such that one glycoside linkage is formed by the corresponding one transferase. Hence, glycosyltransferases are used for structural studies of sugar moiety of complex carbohydrate, for facilitated synthesis of a particular sugar chain structure, and for modification of native sugar chain structure.

Besides, glycosyltransferases are expected to be usable for the modification of the nature of complex carbohydrate and cells, by means of artificial alteration of sugar chain. For this end, the development of various glycosyltransferases having identified substrate specificity has been awaited.

An α1-6 fucosyltransferase is an important enzyme found in Golgi

appratus of organelle, which is considered to be one of the enzymes that control processing of asparagine-linked sugar chain. Therefore, the enzyme will be useful for the elucidation of control mechanism and control of formation of sugar chain structure, once acted on an asparagine-linked sugar chain.

In addition, the activity of α1-6 fucosyltransferase and the proportion of reaction products of this enzyme are known to increase in certain diseases such as liver cancer and cystic fibrosis. Therefore, a rapid development of the method for diagnosis of these diseases has been desired, which involves determination of the activity of this enzyme, Northern blot using a cDNA encoding α1-6 fucosyltransferase, or RT-PCR assay of mRNA amount transcribed and expressed in the living body.

The activity of α1-6 fucosyltransferases has been detected in body fluids or organs of various animals and culture cells thereof, and there has been known, as a purified enzyme product, an enzyme derived from human cystic fibrosis cell homogenates [Journal of Biological Chemistry, vol. 266, pp. 21572-21577 (1991)]. According to this report, however, the enzyme is associated with drawbacks in that (1) its optimum pH is 5.6 which is different from physiological pH, (2) it has relatively low molecular weights (34,000 and 39,000) by SDS-polyacrylamide gel electrophoresis, (3) its large scale and stable supply is practically unattainable due to its being derived from human cell, and others.

This enzyme is obtained as a membrane-bound enzyme, and requires bovine serum for culturing the cells, which in turn results in difficult purification of the enzyme and a huge amount of money necessary for culture of the cells to be a starting material. Consequently, stable supply of this enzyme preparation is all but impractical.

While a chemical synthesis is often employed for synthesizing a sugar chain, the synthesis of oligosaccharides requires many steps that have been necessitated by its complicated synthesis route and specificity of the reaction, so that it involves various practical

problems. Particularly, binding of fucose to GlcNAc bound to Asn of asparagine-linked sugar chain by α1→6 linkage is extremely difficult due to the instability of fucose.

Disclosure of the Invention

It is therefore an object of the present invention to stably provide an α1-6 fucosyltransferase in large amounts, which is useful as a reagent for structural analysis of sugar chain or glyco-technology, or as diagnostics.

Another object of the present invention is to provide a method of producing α1-6 fucosyltransferase in large amounts by the use of a human- or porcine-derived α1-6 fucosyltransferase gene. It is aimed to use such specific genes so as to enable development of a method for diagnosis of diseases by Northern blot using a DNA encoding said enzyme, or by RT-PCR assay of mRNA amount transcribed and expressed in the living body.

In an attempt to achieve the above-mentioned objects, the present inventors started the study of an enzyme capable of linking fucose to GlcNAc linked to Asn of asparagine type sugar chain by α1→6 linkage, using a fluorescence-labeled substrate analogous to an asparagine type sugar chain which is a receptor of this enzyme. As a result, they have found the activity of this enzyme in the extract fractions of porcine brain which is readily available as a starting material to be purified, and they have purified said enzyme from said fractions and elucidated the enzymatic and physico-chemical properties, which resulted in the completion of the invention.

Accordingly, the present invention relates to a porcine-derived α1-6 fucosyltransferase having the following physico-chemical properties (hereinafter this enzyme is referred to as porcine α1-6 fucosyltransferase).

(1) Action: transferring fucose from guanosine diphosphate-fucose to the hydroxy group at 6-position of GluNAc closest to R of a receptor (GlcNAcβ1-2Manα1-6)(GlcNAcβ1-2Manα1-3)Manβ1-4GlcNAcβ1-4GlucNAc-R wherein R is an asparagine residue or a peptide chain

carrying said residue, whereby to form (GlcNAcβ1-2Manα1-6)-(GlcNAcβ1-2Manα1-3)Manβ1-4GlcNAcβ1-4(Fucα1-6)GlucNAc-R.

In the above formula, asparagine residue at R is a residue wherein the acid amide group at the side chain of asparagine is bound to the hydroxy group at the anomer position of the reducing terminal of sugar chain, and a peptide chain having said residue is a peptide chain having said residue in the peptide to which two or more amino acids are bound, which is preferably a peptide chain having -Asn-(X)-Ser/Thr-.

(2) optimum pH : about 7.0

(3) pH stability : stable in the pH range of 4.0-10.0 by treatment at 4℃ for 5 hours

(4) optimum temperature : about 30-37℃

(5) inhibition or activation : no requirement for divalent metal ion for expression of activity; no inhibition of activity even in the presence of 5 mM EDTA

(6) molecular weight : about 60,000 by SDS-polyacrylamide gel electrophoresis.

The present inventors have purified α1-6 fucosyltransferase alone from porcine brain, analyzed the amino acid sequence of this protein and cloned a gene based on the partial amino acid sequence to accomplish the present invention.

That is, the present invention provides a gene encoding porcine α1-6 fucosyltransferase.

The present invention also provides an expression vector containing a gene encoding porcine α1-6 fucosyltransferase.

The present invention further provides a transformant cell obtained by transforming a host cell with an expression vector containing a gene encoding porcine α1-6 fucosyltransferase.

The present invention yet provides a method for producing a recombinant α1-6 fucosyltransferase, comprising culturing a transformant cell obtained by transforming a host cell with an expression vector containing a gene encoding porcine α1-6 fucosyltransferase, and harvesting the α1-6 fucosyltransferase from the

culture thereof.

The present inventors have reached the present invention by purifying protein having an α1-6 fucosyltransferase activity from human cell culture broth and elucidating its enzymatic property.

Accordingly, the present invention relates to an α1-6 fucosyltransferase derived from human, having the following physico-chemical property (hereinafter this enzyme is to be referred to as human α1-6 fucosyltransferase).

(1) Action: transferring fucose from guanosine diphosphate-fucose to the hydroxy group at 6-position of GluNAc closest to R of a receptor (GlcNAcβ1-2Manα1-6)(GlcNAcβ1-2Manα1-3)Manβ1-4GlcNAcβ1-4GlucNAc-R wherein R is an asparagine residue or a peptide chain carrying said residue, whereby to form (GlcNAcβ1-2Manα1-6)-(GlcNAcβ1-2Manα1-3)Manβ1-4GlcNAcβ1-4(Fucα1-6)GlucNAc-R.

In the above formula, asparagine residue at R is a residue wherein the acid amide group at the side chain of asparagine is bound to the reducing terminal hydroxy group of sugar chain, and a peptide chain having said residue is a peptide chain having said residue in the peptide to which two or more amino acids are bound, which is preferably a peptide chain having -Asn-(X)-Ser/Thr-.

(2) optimum pH : about 7.5

(3) pH stability : stable in the pH range of 4.0-10.0 by treatment at 4°C for 5 hours

(4) optimum temperature : about 30-37°C

(5) inhibition or activation : no requirement for divalent metal ion for expression of activity; no inhibition of activity even in the presence of 5 mM EDTA

(6) molecular weight : about 60,000 by SDS-polyacrylamide gel electrophoresis.

The present inventors have purified α1-6 fucosyltransferase alone from human culture cell, analyzed the amino acid sequence of this protein and cloned a gene based on the partial amino acid sequence to accomplish the present invention.

That is, the present invention provides a gene encoding human α1-6 fucosyltransferase.

The present invention also provides an expression vector containing a gene encoding human α1-6 fucosyltransferase.

The present invention further provides a transformant cell obtained by transforming a host cell with an expression vector containing a gene encoding human α1-6 fucosyltransferase.

The present invention yet provides a method for producing a recombinant α1-6 fucosyltransferase, comprising culturing a transformant cell obtained by transforming a host cell with an expression vector containing a gene encoding human α1-6 fucosyltransferase, and harvesting the α1-6 fucosyltransferase from the culture thereof.

The starting material for the purification of the enzyme of the present invention is, for example, the organ and body fluid of pig having α1-6 fucosyltransferase activity. Examples of the organ include brain, spermary, pancreas, lung, kidney and the like. The body fluid of pig such as blood and sera can be also used.

The porcine α1-6 fucosyltransferase of the present invention can be obtained by preparing a crude extract containing the enzyme from, for example, homogenates of porcine brain and separating the enzyme from this extract. In this case, since α1-6 fucosyltransferase in the porcine brain is a membrane-bound enzyme, a crude extract solution containing the enzyme is generally obtained from brain lysate using a suitable surfactant. This extract undergoes various known purification steps to give a purified enzyme product. The purification may include, for example, concentration using an ultrafiltration membrane, desalting, affinity column chromatography wherein a substrate analog is immobilized, ion exchange column chromatography, hydrophobic column chromatography and the like in suitable combination to give a substantially homogeneous enzyme product which is free of contaminant proteins such as other transferases. For example, porcine brain is disrupted in a Waring blender in a phosphate buffer and membrane

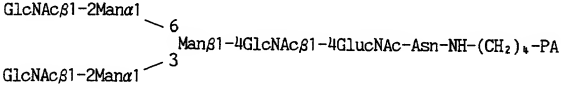
fractions are collected by ultracentrifugation. The objective enzyme is extracted with a phosphate buffer containing a surfactant (Triton X-100), and the supernatants are collected by ultracentrifugation to give a crude extract containing the enzyme. By applying affinity column chromatography using a guanosine diphosphate (GDP)-hexanolamine-sepharose, a GlcNAcβ1-2Manα1-6(GlcNAcβ1-2Manα1-3)Manβ1-4GlcNAcβ1-4GlcNAc-asparagine-sepharose and the like, the fractions showing fucosyltransferase activity are collected and purified.

The physico-chemical property of α1-6 fucosyltransferase derived from porcine brain, which is one aspect of the present invention, is as follows.

(1) Action: transferring fucose from guanosine diphosphate-fucose to the hydroxy group at 6-position of GluNAc closest to R of a receptor (GlcNAcβ1-2Manα1-6)(GlcNAcβ1-2Manα1-3)Manβ1-4GlcNAcβ1-4GlucNAc-R wherein R is an asparagine residue or a peptide chain carrying said residue, whereby to form (GlcNAcβ1-2Manα1-6)-(GlcNAcβ1-2Manα1-3)Manβ1-4GlcNAcβ1-4(Fucα1-6)GlucNAc-R.

(2) Determination of activity:

The activity of the porcine α1-6 fucosyltransferase was determined as follows. That is, a compound of the following formula, wherein the sugar chain end asparagine was fluorescence-labeled with 4-(2-pyridylamino)butylamine [PABA: $-NH_2(CH_2)_4-NH$-pyridine] was used as a substrate for determination of enzyme activity:



wherein PA means pyridylamino. By the use of this substrate, the product from the enzyme reaction, wherein fucose has been transferred by α1→6 linkage, can be assayed by detecting fluorescence by high performance liquid chromatography.

Specifically, the determination includes the following steps. A sample solution (10 μl) and 1.25% Triton X-100 are added to a 250 mM

MES buffer containing 62.5 μM of fluorescence-labeled receptor substrate of the above formula and 625 μM of a donor substrate (GDP-fucose), pH 7.0, 40 μl, and mixed. The mixture is reacted at 37°C for one hour, and boiled for 5 minutes to stop the reaction. The reaction mixture is subjected to high performance liquid chromatography and the peak of the reaction product is assayed with a fluorescence detector. One unit of the enzyme amount corresponds to the amount capable of forming 1 pmole of GlcNAc β1-2Manα1-6(GlcNAcβ1-2Manα1-3)Manβ1-4GlcNAcβ1-4(Fucα1-6)GlcNAc-R (wherein R is Asn-NH-$(CH_2)_4$-NH-pyridine) in one minute under these conditions.

(3) Optimum pH:

The α1-6 fucosyltransferase derived from porcine brain (hereinafter this enzyme is referred to as porcine brain α1-6 fucosyltransferase) shows a high activity at nearly pH 7.0-7.5.

(4) pH Stability:

The porcine brain α1-6 fucosyltransferase is relatively stable at pH 4-10, and more stable at pH 5-9.

(5) Optimum temperature:

The porcine brain α1-6 fucosyltransferase has an optimum temperature at nearly 37°C and retains sufficient activity at 20-40°C.

(6) Divalent metal ion requirement:

The porcine brain α1-6 fucosyltransferase shows sufficient activity even in the absence of divalent metal ion, such as magnesium, manganese and the like. It also shows sufficient activity even in the presence of 5 mM EDTA, which is a chelating agent.

(7) Molecular weight:

A purified product of the porcine brain α1-6 fucosyltransferase shows a single band at a molecular weight of about 60,000 by SDS-polyacrylamide gel electrophoresis.

Judging from the above properties, the porcine brain α1-6 fucosyltransferase is a novel enzyme apparently different from conventionally known α1-6 fucosyltransferase derived from human cystic fibrosis cells (optimum pH 5.6, molecular weights 34,000 and 39,000),

in terms of optimum pH, metal ion requirement and molecular weight.

The inventive porcine α1-6 fucosyltransferase is expected to be extremely useful for (1) synthesis of sugar chain compounds wherein sugar chain compounds having 1-6 fucose are synthesized using the enzyme of the present invention, (2) modification of sugar chain structure and functional analysis wherein a fucose is newly introduced into asparagine type sugar chain to artificially modify the sugar chain structure, whereby changes in cell function and control mechanism of the processing of complex carbohydrate, as well as the role of sugar chain, can be elucidated, (3) diagnosis of lesions based on enzyme activity wherein diseases such as cancer can be diagnosed by determining the activity of the enzyme of the present invention which reflects various lesions caused by tumorigenic transformation, (4) diagnosis of various diseases wherein a specific antibody against the enzyme of the present invention is prepared and used for the diagnosis, and the like.

Another aspect of the present invention is a gene encoding porcine α1-6 fucosyltransferase, which includes a gene encoding α1-6 fucosyltransferase and including a gene encoding amino acid sequence depicted in Sequence Listing, SEQ ID NO:2. A different embodiment thereof is a gene encoding α1-6 fucosyltransferase and including nucleotide sequence depicted in Sequence Listing, SEQ ID NO:1.

One aspect of the present invention is a gene encoding porcine α1-6 fucosyltransferase and including a gene encoding an amino acid sequence resulting from substitution, insertion, deletion or addition with respect to at least one amino acid of the amino acid sequence depicted in Sequence Listing, SEQ ID NO:2.

Another aspect of the present invention is a gene encoding porcine α1-6 fucosyltransferase and including a nucleotide sequence resulting from substitution, insertion, deletion or addition with respect to at least one nucleotide of the nucleotide sequence depicted in Sequence Listing, SEQ ID NO:1.

The present invention also includes, as one aspect thereof, a gene that hybridizes to at least a part of a gene encoding porcine α1-6

fucosyltransferase and including nucleotide sequence depicted in Sequence Listing, SEQ ID NO:1.

The expression vector of the present invention contains a gene encoding the above-mentioned porcine α1-6 fucosyltransferase.

The transformant host cell of the present invention has been transformed with the above-mentioned expression vector.

The host cell is exemplified by microorganisms, such as *Escherichia coli*, yeast, bacterial cells and the like. It also includes animal cells such as insect cells, COS-1 cells, CHO cells and the like, and plant cells, such as tobacco cells, *Arabidopsis* cells and the like.

The vector may be any which is selected according to the host to be transformed. In the case of *Escherichia coli*, for example, pUC19 may be used; in the case of yeast, pYEUra3™ may be used; in the case of insect cells, pBLUE Bac4 may be used; in the case of COS-1 cells, pSVK3 may be used; and in the case of tobacco cells and *Arabidopsis* cells, pBI may be used.

The method for preparing the inventive recombinant α1-6 fucosyltransferase includes culturing the above-mentioned transformant cells and harvesting α1-6 fucosyltransferase from the culture.

According to the present invention, α1-6 fucosyltransferase alone is purified from porcine brain, and subjected to amino acid analysis of this protein. Its partial amino acid sequence is determined and a primer for PCR is prepared based on the amino acid sequence. Using this primer, PCR is performed using cDNAs derived from porcine brain as a template to amplify a gene encoding α1-6 fucosyltransferase to give a probe. This probe is used to screen clones containing cDNA encoding α1-6 fucosyltransferase, from the cDNA library derived from porcine brain. The cDNA encoding α1-6 fucosyltransferase is isolated and used to express α1-6 fucosyltransferase.

To be specific, the purified porcine α1-6 fucosyltransferase is used to analyze amino acid sequences. For example, SDS-polyacrylamide gel electrophoresis is applied, after which the protein is transferred to PVDF membrane by electroblotting, and the PVDF membrane containing

ca. 60 kDa band is cut out and subjected to sequencing using a protein sequencer. As a result, the amino acid sequence of the amino terminal of α1-6 fucosyltransferase depicted in Sequence Listing, SEQ ID NO:3 is obtained.

Separately, purified α1-6 fucosyltransferase is subjected to SDS-polyacrylamide gel electrophoresis and the peptide fragments separated by electrophoresis are transferred to PVDF membrane by electroblotting. Then, the PVDF membrane containing 60 kDa band is cut out and lysed on said PVDF membrane, using, for example, a protease such as lysylendopeptidase. The lysate is extracted from the sections of said PVDF membrane, and the extract is subjected to reversed phase high performance liquid chromatography to separate the lysate.

Then, using the amino acid sequences, a mixed primer for PCR is prepared. For example, a mixed primer having a nucleotide sequence depicted in SEQ ID NO:7 is synthesized from the amino acid sequence depicted in SEQ ID NO:3, and a mixed primer having a nucleotide sequence depicted in SEQ ID NO:8 is synthesized from the amino acid sequence depicted in SEQ ID NO:4, respectively using a DNA synthesizer, and used for the screening of cDNA of α1-6 fucosyltransferase.

For example, 25 cycles of PCR are performed to amplify DNA fragments of ca. 1.45 kbp, using cDNA from porcine brain as a template and mixed primers of SEQ ID NO:7 and SEQ ID NO:8, wherein PCR at 94°C (1 min), 55°C (2 min) and 72°C (3 min) is one cycle.

Then, using the amplified DNA fragments as a probe, clones containing cDNA encoding α1-6 fucosyltransferase are screened from the cDNA library derived from porcine brain by a plaque hybridization method. The cDNA encoding α1-6 fucosyltransferase can be isolated from the obtained clones. The nucleotide sequence of the obtained cDNA and the amino acid sequence deduced from said nucleotide sequence are shown in SEQ ID NO:1 and SEQ ID NO:2.

Said cDNA is subcloned into an expression vector such as pSVK3. The host cells, such as COS-1 cells, transformed with said subcloned plasmid, are cultured and α1-6 fucosyltransferase is obtained from the

culture.

In the present invention, the above-mentioned transformant cells are cultured and α1-6 fucosyltransferase is harvested from the culture, whereby recombinant α1-6 fucosyltransferase is obtained. The method for harvesting the enzyme from the culture is a conventional one.

The gene encoding the porcine α1-6 fucosyltransferase of the present invention and DNA fragments (which are the lysates thereof) may be used for the detection of the expression of α1-6 fucosyltransferase in the living body, and thus are useful for the genetic diagnosis of certain diseases such as liver cancer and cystic fibrosis.

In addition, the polypeptide that is encoded by these genes can be used to immunologically prepare various antibodies which are useful for diagnosis and purification of α1-6 fucosyltransferase.

The starting material for the purification of the enzyme in this invention may be any as long as it is a human cell culture medium exhibiting α1-6 fucosyltransferase activity. For example, human pancreatic cancer cells, human gastric cancer cells, human myeloma tumor cells and the like may be used as the cells having α1-6 fucosyltransferase activity.

While the human α1-6 fucosyltransferase is present in the cell membrane as a membrane-bound enzyme, it is cleaved by protease at a site unaffecting the enzyme activity and released into the culture medium as a soluble enzyme. Thus, the culture medium can be used as a crude enzyme solution, without complicated steps such as disruption of cells and solubilizing of the enzyme. Besides, the use of cells capable of growth in serum-free media enables economical production of a crude enzyme solution having a high purity. The culture medium is concentrated and desalted, and subjected to ion exchange chromatography, affinity chromatography and the like to give a purified enzyme product free of contaminant transferases and glycosidase activity.

α1-6 Fucosyltransferase is purified from human gastric cancer cells by, for example, culturing human gastric cancer cell MKN45 without

serum and purifying the enzyme from the obtained culture medium. In this case, α1-6 fucosyltransferase of human gastric cancer cell MKN45 is cleaved by protease in the cells at a site unaffecting the enzyme activity and released into culture medium as a soluble α1-6 fucosyltransferase. Therefore, the culture medium can be used as a crude enzyme solution, without complicated steps such as disruption of cells and solubilizing of the enzyme with a surfactant. The crude enzyme solution is subjected to known purification steps to give a purified enzyme product.

In the present invention, a serum-free culture medium of human gastric cancer cell MKN45 is concentrated by filtration through an ultrafiltration membrane, and then the buffer is changed to a Tris-HCl buffer containing 5 mM 2-mercaptoethanol and 0.1% CHAPS [3-((3-cholamidopropyl)dimethylammonio)-1-propanesulfonate], pH 7.5, to give a crude enzyme solution.

This enzyme solution is subjected to column chromatography using Q-sepharose, GDP-hexanolamine-sepharose, (GlcNAcβ1-2Manα1-6)(GlcNAcβ1-2Manα1-3)Manβ1-4GlucNAcβ1-4GlucNAc-asparagine-sepharose and the like to collect active fractions, from which the fucosyltransferase of the present invention can be purified.

The physico-chemical property of human α1-6 fucosyltransferase of the present invention is as follows.

(1) Action: transferring fucose from guanosine diphosphate-fucose to the hydroxy group at 6-position of GluNAc closest to R of a receptor (GlcNAcβ1-2Manα1-6)(GlcNAcβ1-2Manα1-3)Manβ1-4GlcNAcβ1-4GlucNAc-R wherein R is an asparagine residue or a peptide chain carrying said residue, whereby to form (GlcNAcβ1-2Manα1-6)-(GlcNAcβ1-2Manα1-3)Manβ1-4GlcNAcβ1-4(Fucα1-6)GlucNAc-R.

(2) Determination of enzyme activity:

The activity of the human α1-6 fucosyltransferase was determined as follows. That is, a compound of the above-mentioned formula, wherein the asparagine on the end of sugar chain was fluorescence-labeled with 4-(2-pyridylamino)butylamine [PABA: $-NH_2(CH_2)_4-NH-$

pyridine], was used as a substrate for determination of enzyme activity. By the use of this substrate, the product from the enzyme reaction, wherein fucose is transferred by α1→6 linkage, can be assayed by detecting fluorescence by high performance liquid chromatography.

Specifically, the determination included the following steps. An enzyme solution (10 µl) was added to a 250 mM MES buffer containing 62.5 µM of fluorescence-labeled receptor substrate of the above formula and 625 µM of a donor substrate (GDP-fucose), pH 7.0, 40 µl, and mixed. The mixture was reacted at 37°C for one hour, and boiled for 5 minutes to stop the reaction. The reaction mixture is subjected to high performance liquid chromatography and the peak of the reaction product is assayed with a fluorescence detector.

One unit of the enzyme amount corresponded to the amount capable of producing 1 pmole of GlcNAcβ1-2Manα1-6(GlcNAcβ1-2Manα1-3)-Manβ1-4GlcNAcβ1-4(Fucα1-6)GlcNAc-R (wherein R is Asn-NH-$(CH_2)_4$-NH-Pyridine) in one minute under these conditions.

(3) Optimum pH:

The human α1-6 fucosyltransferase shows high activity at nearly pH 7.0-7.5, as shown by a curve in Fig. 1. In Fig. 1, the determination was performed using 500 mM MES buffer (black circle) at pH 4.5-7.5 and 100 mM Tris-HCl buffer (white circle) at pH 7.0-9.0.

(4) pH Stability:

The human α1-6 fucosyltransferase is stable at about pH 4-10, particularly at pH 5-9, as shown in Fig. 2. The buffers used for the determination were 50 mM acetate buffer (black triangle) at pH 3.5-5.5, 50 mM MES buffer (black circle) at pH 5.5-7.5, 50 mM Tris-HCl buffer (white circle) at pH 7.5-9.0, and sodium hydrogencarbonate buffer (white triangle) at pH 9.0-11.5. The enzyme of the present invention was treated in each buffer at each pH at 4°C for 5 hours, and the residual activity was determined. Fig. 1 is a graph showing the relationship between pH (axis of abscissa) and relative activity (%, axis of ordinate) of the human α1-6 fucosyltransferase obtained by the

present invention, and Fig. 2 is a graph showing pH (axis of abscissa) and residual activity (%, axis of ordinate).

(5) Optimum temperature:

The human α1-6 fucosyltransferase has an optimum temperature at nearly 37°C as shown in Fig. 3 and is usable at 20-40°C. A frozen product thereof is stable at -20°C for at least several months.

(6) Divalent metal ion requirement:

Many glycosyltransferases require divalent metal ion for their activity, such as magnesium, manganese and the like. This human α1-6 fucosyltransferase shows sufficient activity in the absence of divalent metal ion or in the presence of EDTA, which is a chelating agent, and does not require divalent metal ion.

(7) Molecular weight:

A purified product of the human α1-6 fucosyltransferase of the present invention shows a single band at a molecular weight of about 60,000 by SDS-polyacrylamide gel electrophoresis.

(8) Morphology:

While the human α1-6 fucosyltransferase is intrinsically present in cell membrane as a membrane-bound enzyme, it is cleaved by protease in the cultured cell at a site unaffecting the enzyme activity and released into a culture medium as a soluble enzyme permitting easy handling, unlike porcine-derived α1-6 fucosyltransferase and α1-6 fucosyltransferase derived from human cystic fibrosis cells heretofore reported.

Judging from the above properties, the human α1-6 fucosyltransferase is a novel enzyme apparently different from conventionally known α1-6 fucosyltransferase derived from human cystic fibrosis cells (optimum pH 6.5, molecular weights 34,000 and 39,000), in terms of optimum pH, metal requirement and molecular weight.

The human α1-6 fucosyltransferase is used for the following purposes.

(1) Artificial modification of sugar chain structure by introducing fucose anew into the asparagine-linked sugar chain, whereby cell

apparatus and control mechanism of processing of sugar chain of complex carbohydrate, as well as the role of sugar chain, can be elucidated.
(2) Diagnosis of various diseases based on the activity of the inventive enzyme.
(3) Diagnosis of various diseases wherein a specific antibody against the enzyme of the present invention is prepared and used for the diagnosis.

The present invention is a gene encoding human α1-6 fucosyltransferase, which includes, as one embodiment, a gene encoding α1-6 fucosyltransferase and including a gene encoding an amino acid sequence depicted in Sequence Listing, SEQ ID NO:10. A different embodiment thereof is a gene encoding α1-6 fucosyltransferase inclusive of nucleotide sequence depicted in Sequence Listing, SEQ ID NO:9. A further aspect of the present invention is a gene encoding α1-6 fucosyltransferase and including a nucleotide sequence from 198th adenine to 1919th guanine as depicted in Sequence Listing, SEQ ID NO:9.

One aspect of the present invention is a gene encoding α1-6 fucosyltransferase and including a gene encoding an amino acid sequence resulting from substitution, insertion, deletion or addition with respect to at least one amino acid of the amino acid sequence depicted in Sequence Listing, SEQ ID NO:10.

Another aspect of the present invention is a gene encoding α1-6 fucosyltransferase and including a nucleotide sequence resulting from substitution, insertion, deletion or addition with respect to at least one nucleotide of the nucleotide sequence depicted in Sequence Listing, SEQ ID NO:9.

The present invention also includes, as one embodiment, a gene which hybridizes to at least a part of gene encoding α1-6 fucosyltransferase and including nucleotide sequence depicted in Sequence Listing, SEQ ID NO:9.

The expression vector of the present invention contains a gene encoding the above-mentioned α1-6 fucosyltransferase.

The transformant host cell of the present invention has been

transformed with the above-mentioned expression vector.

The host cell is exemplified by microorganisms, such as *Escherichia coli*, yeast, bacterial cells and the like. It also includes animal cells such as insect cells, COS-1 cells, CHO cells and the like, and plant cells, such as tobacco cells, *Arabidopsis* cells and the like.

The vector may be any which is selected according to the host to be transformed. In the case of *Escherichia coli*, for example, pUC19 may be used; in the case of yeast, pYEUra3™ may be used; in the case of insect cells, pBLUE Bac4 may be used; in the case of COS-1 cells, pSVK3 may be used; and in the case of tobacco cells and *Arabidopsis* cells, pBI may be used.

The method for preparing the recombinant α1-6 fucosyltransferase includes culturing the above-mentioned transformant cells and harvesting α1-6 fucosyltransferase from the culture.

According to the present invention, α1-6 fucosyltransferase alone is purified from human gastric cancer cells, and subjected to amino acid analysis of this protein. Its partial amino acid sequence is determined and a primer for PCR is prepared based on the amino acid sequence. Using this primer, PCR is performed using cDNAs derived from human gastric cancer cells as a template to amplify a gene encoding α1-6 fucosyltransferase to give a probe. This probe is used to screen clones containing cDNA encoding α1-6 fucosyltransferase, from the cDNA library derived from human gastric cancer cells. The cDNA encoding α1-6 fucosyltransferase is isolated and used to express α1-6 fucosyltransferase.

To be specific, the purified α1-6 fucosyltransferase is used to analyze amino acid sequence. For example, it is subjected to SDS-polyacrylamide gel electrophoresis, after which the protein is transferred to PVDF membrane by electroblotting, and the PVDF membrane containing ca. 60 kDa band is cut out and subjected to sequencing by a protein sequencer. As a result, the amino acid sequence of the amino terminal of α1-6 fucosyltransferase depicted in Sequence Listing, SEQ ID NO:11 is obtained.

Separately, purified α1-6 fucosyltransferase is subjected to SDS-polyacrylamide gel electrophoresis, along with a protease such as lysylendopeptidase, and the peptide fragments separated by electrophoresis are transferred to PVDF membrane by electroblotting. Then, the band containing the peptide fragments is cut out and subjected to sequencing with a protein sequencer. Thus, partial amino acid sequences of α1-6 fucosyltransferase as depicted in Sequence Listing, SEQ ID NO:12 and SEQ ID NO:13 are obtained. Then, using these amino acid sequences, a mixed primer for PCR is prepared. For example, a mixed primer having a nucleotide sequence depicted in SEQ ID NO:14 is synthesized from the amino acid sequence depicted in SEQ ID NO:12, and a mixed primer having a nucleotide sequence depicted in SEQ ID NO:15 is synthesized from the amino acid sequence depicted in SEQ ID NO:13, respectively using a DNA synthesizer, and used for the screening of cDNA of α1-6 fucosyltransferase.

For example, 36 cycles of PCR are performed to amplify the DNA fragments of ca. 200 bp, using cDNA from human gastric cancer cells as a template and mixed primers of SEQ ID NO:14 and SEQ ID NO:15, wherein PCR at 94°C (30 sec), 46°C (30 sec) and 72°C (1.5 min) is one cycle.

Then, using the amplified DNA fragments as a probe, clones containing cDNA encoding α1-6 fucosyltransferase are screened from the cDNA library derived from human gastric cancer cells by a plaque hybridization method. The cDNA encoding α1-6 fucosyltransferase can be isolated from the obtained clones. The nucleotide sequence of the obtained cDNA and the amino acid sequences deduced from said nucleotide sequence are shown in SEQ ID NO:9 and SEQ ID NO:10.

Said cDNA is subcloned into an expression vector such as pSVK3. The host cells such as COS-1 cells transformed with said subcloned plasmid are cultured and α1-6 fucosyltransferase is obtained from the culture.

In the present invention, the above-mentioned transformant cells are cultured and α1-6 fucosyltransferase is harvested from the culture, whereby a recombinant α1-6 fucosyltransferase is obtained.

The method for harvesting the enzyme from the culture is a conventional one.

The gene encoding the human α1-6 fucosyltransferase of the present invention and DNA fragments (which are the lysates thereof) may be used for the determination of the expression of α1-6 fucosyltransferase in the living body and thus are useful for genetic diagnosis of certain diseases such as liver cancer and cystic fibrosis.

In addition, the polypeptide that is encoded by these genes can be used to immunologically prepare various antibodies which are useful for diagnosis and purification of α1-6 fucosyltransferase.

Brief Description of the Drawings

Fig. 1 shows optimum pH of the porcine brain α1-6 fucosyltransferase of the present invention.

Fig. 2 shows pH stability of the porcine brain α1-6 fucosyltransferase of the present invention.

Fig. 3 shows optimum temperature of the porcine brain α1-6 fucosyltransferase of the present invention.

Fig. 4 shows optimum pH of the human α1-6 fucosyltransferase of the present invention.

Fig. 5 shows pH stability of the human α1-6 fucosyltransferase of the present invention.

Fig. 6 shows optimum temperature of the human α1-6 fucosyltransferase of the present invention.

Embodiment of the Invention

The present invention is described in more detail by way of Examples.

In the present invention, the enzyme activity is determined as follows.

A compound of the following formula, wherein the asparagine on the end of sugar chain had been fluorescence-labeled with 4-(2-pyridylamino)butylamine [PABA: $-NH(CH_2)_4-NH$-pyridine] was used as a substrate for the determination of enzyme activity.

By the use of this substrate, the product from the enzyme reaction wherein fucose has been transferred by $\alpha 1 \rightarrow 6$ linkage can be assayed by detecting the fluorescence by high performance liquid chromatography.

Specifically, the determination includes the following steps. A sample solution (10 µl) and 1.25% Triton X-100 are added to a 250 mM MES buffer containing 62.5 µM of fluorescence-labeled receptor substrate of the above formula and 625 µM of a donor substrate (GDP-fucose), pH 7.0, 40 µl, and mixed. The mixture is reacted at 37°C for one hour, and boiled for 5 minutes to stop the reaction. The reaction mixture is subjected to high performance liquid chromatography and the peak of the reaction product is assayed with a fluorescence detector. One unit of the enzyme amount corresponds to the amount capable of producing 1 pmole of GlcNAcβ1-2Manα1-6(GlcNAcβ1-2Manα1-3)-Manβ1-4GlcNAcβ1-4(Fucα1-6)GlcNAc-R (wherein R is Asn-NH-$(CH_2)_4$-NH-pyridine) in one minute under these conditions.

Example 1

(1) Preparation of porcine brain lysate and crude extract solution

Porcine brain (100 g) was disrupted in a Waring blender in a 20 mM potassium phosphate buffer (pH 7.0) and membrane fractions were collected by ultracentrifugation. The membrane fractions were extracted with the same buffer containing Triton X-100 (concentration 0.5%) to extract the enzyme. After the extraction, the supernatants were collected by centrifugation to give an extract containing a crude enzyme.

(2) Purification of enzyme from crude extract solution

A GlcNAcβ1-2Manα1-6(GlcNAcβ1-2Manα1-3)Manβ1-4GlcNAcβ1-4GlcNAc-asparagine-sepharose column (column of asialoagalactoglycopeptide derived from transferrin) was equilibrated with a 20 mM

potassium phosphate buffer (pH 7.0) containing 0.05% Triton X-100 and 50 mM KCl, and the crude extract solution prepared in (1) above was applied. The column was washed with said buffer until the protein was not detected in the unadsorbed fractions. The active fractions were eluted with the same buffer containing 1M KCl. Then, the active fractions of the enzyme were concentrated using an ultrafiltration membrane and desalted, and applied to a GDP-hexanolamine-sepharose column equilibrated with the same buffer. The elution was performed using the same buffer containing 100 mM GDP. Then, the active fractions were collected and concentrated using an ultrafiltration membrane, and desalted to give porcine brain α1-6 fucosyltransferase. The porcine brain α1-6 fucosyltransferase thus obtained showed a single band at a molecular weight of about 60,000 by SDS-polyacrylamide gel electrophoresis. No other bands ascribed to impurities were found and the enzyme was free of other transferase activities, thus indicating that the enzyme obtained was highly purified.

The optimum pH (determined by changing the pH of buffer) of the enzyme of the present invention is shown in Fig. 1. The enzyme showed high activity at around pH 7.0-7.5. The buffer used was 200 mM MES buffer (black circle). In this graph, the axis of abscissa shows pH of α1-6 fucosyltransferase obtained in the present invention and the axis of ordinate shows relative activity (%).

The pH stability of the enzyme of the present invention was examined in the same manner. Fig. 2 shows residual activity after treating the enzyme in each buffer at each pH, 4°C for 5 hours. The enzyme was comparatively stable at about pH 4-10, and particularly stable at pH 5-9. The buffers used were 50 mM acetate buffer (black triangle) at pH 3.5-5.5, 50 mM MES buffer (black circle) at pH 5.5-7.5, 50 mM Tris-HCl buffer (white circle) at pH 7.5-9.0, and sodium hydrogencarbonate buffer (white triangle) at pH 9.0-11.5. The axis of abscissa of the graph shows pH of α1-6 fucosyltransferase obtained in the present invention and the axis of ordinate shows residual activity (%).

As shown in Fig. 3, the optimum temperature of the enzyme of the present invention was found to be at about 37°C and the enzyme was considered to retain sufficient activity in the range of 20-40°C. A frozen product thereof was stable at -20°C for at least several months. The buffer used was 200 mM MES buffer (black circle), pH 7.0. The axis of abscissa of the graph shows treatment temperature (°C) and the axis of ordinate shows relative activity (%) of the α1-6 fucosyltransferase obtained in the present invention.

While many glycosyltransferases require divalent metal ion for their activity, such as magnesium, manganese and the like, the enzyme showed sufficient activity in the absence of such divalent metal ion. Inasmuch as it showed sufficient activity even in the presence of 5 mM EDTA, which is a chelating agent, it is concluded that the enzyme does not require a divalent metal ion.

Example 2

Determination of amino terminal amino acid sequence of porcine brain α1-6 fucosyltransferase

Purified porcine brain α1-6 fucosyltransferase (5 μg) was subjected to SDS-polyacrylamide gel electrophoresis, after which the protein was transferred to PVDF membrane (Millipore) by electroblotting. The PVDF membrane was stained with Coomassie Brilliant Blue G250, and a single band of porcine brain α1-6 fucosyltransferase was detected at 60 kDa.

Then, the PVDF membrane containing said band was cut out, and, after destaining with 50% methanol, subjected to Biosystem 473A protein sequencer (Applied Biosystems) to determine amino terminal amino acid sequence of α1-6 fucosyltransferase. The amino acid sequence determined is depicted in Sequence Listing, SEQ ID NO:3.

Example 3

Determination of partial amino acid sequence of porcine brain α1-6 fucosyltransferase

Purified porcine brain α1-6 fucosyltransferase (13 μg) was subjected to SDS-polyacrylamide gel electrophoresis, after which the

protein was transferred to PVDF membrane (Millipore) by electroblotting. The PVDF membrane was stained with Coomassie Brilliant Blue G250, and a single band of porcine brain α1-6 fucosyltransferase was detected at 60 kDa.

Then, the PVDF membrane containing said band was cut out and destained with 50% methanol. Said PVDF membrane section was treated in 100 mM Tris-HCl buffer-5% acetonitrile (pH 8.2) containing 1 μg of lysylendopeptidase, at 37°C for 12 hours for proteolysis. The PVDF membrane section which underwent proteolysis was ultrasonicated to extract the proteolysis product. The proteolysis product thus obtained was separated by a reversed phase high performance liquid chromatography using a C-18 column to give 3 peptide fragments. The substance containing said peptide fragments, which was separated by the reversed phase high performance liquid chromatography, was applied to polybrene-coated precycled glass fiber filter activated with trifluoroacetate and dried, and then subjected to Biosystem 473A protein sequencer (Applied Biosystems) to determine partial amino acid sequence of porcine brain α1-6 fucosyltransferase. The determined amino acid sequence is depicted in Sequence Listing, SEQ ID NOs:4-6.

Example 4

Preparation of probe DNA by PCR

Mixed primers shown in SEQ ID NO:7 and SEQ ID NO:8 were synthesized from the amino acid sequences obtained in Examples 2 and 3. The mixed primer shown in SEQ ID NO:7 was used as a sense primer, and the mixed primer shown in SEQ ID NO:8 was used as an antisense primer for PCR. To be specific, 25 cycles of PCR were performed wherein PCR at 94°C (1 min), 55°C (2 min) and 72°C (3 min) using 2 μg of porcine brain-derived cDNA, 25 pmole of sense primer (mixed primer shown in SEQ ID NO: 7), 25 pmole of antisense primer (mixed primer shown in SEQ ID NO:8) and a reaction mixture (50 μl) of 50 mM potassium chloride-10 mM Tris-HCl buffer (pH 8.3)-1.5 mM magnesium chloride-0.001% gelatin-200 μM dNTP, containing 2.5 units of Taq DNA polymerase was one cycle.

The reaction mixture (10 μl) after PCR was subjected to 0.7%

agarose gel electrophoresis to confirm the PCR reaction product DNA fragments. As a result of PCR performed using a mixed primer shown in SEQ ID NO:7 and a mixed primer shown in SEQ ID NO:8 in combination, a 1.45 kbp DNA fragment was confirmed by agarose gel electrophoresis.

This DNA fragment was subcloned into plasmid pT7BLUEt-Vector (Novagen) and nucleotide sequence was confirmed. As a result, a DNA corresponding to the amino acid sequence depicted in Sequence Listing, SEQ ID NOs:3-6 was detected, whereby the DNA fragment was confirmed to be a part of α1-6 fucosyltransferase gene.

Example 5

Isolation of porcine brain α1-6 fucosyltransferase gene

The DNA fragments obtained in Example 4 were labeled with α-^{32}P dCTP (3000 Ci/mmol, Amersham) and used as a probe to screen clones containing cDNA encoding α1-6 fucosyltransferase, from porcine brain-derived λgt11 cDNA library (Clonetech) by plaque hybridization method.

As a result of screening of about 400,000 plaques, 5 positive clones c1, c2, c3, c4 and c5 were obtained. Said clones c1 and c2 were postulated to contain a full length α1-6 fucosyltransferase gene in view of their length. Thus, the nucleotide sequences of c1 and c2 were determined, and a nucleotide sequence depicted in SEQ ID NO:1 was obtained.

Example 6

Expression of porcine brain α1-6 fucosyltransferase gene

The coding region of α1-6 fucosyltransferase gene was subcloned into expression vector pSVK3 from clones containing cDNA encoding porcine brain α1-6 fucosyltransferase obtained in Example 5. The expression vector containing said α1-6 fucosyltransferase gene was introduced into COS-1 cells. After 48 hours of incubation, culture cells were collected and the cells were disrupted. The enzyme activity of α1-6 fucosyltransferase in the obtained lysate was determined.

As a control, the enzyme activity of α1-6 fucosyltransferase in the lysate of COS-1 cells, into which mock pSVK3 had been introduced,

was determined. As a result, the control hardly showed activity, whereas COS-cells into which the expression vector containing said α1-6 fucosyltransferase gene had been introduced, showed a high activity of 2360 nmole/h/mg protein.

Example 7

(1) Preparation of crude enzyme solution from serum-free culture medium of human gastric cancer cell MKN45

Human gastric cancer cell MKN45 was cultured in a serum-free medium (RPMI1640 medium:Ham's F-12 medium=1:1) containing sodium selenite and canamycin, at 37°C in 5% CO_2. The resulting serum-free culture medium (100 ℓ) was concentrated to 2 ℓ by ultrafiltration. The buffer was changed to a Tris-HCl buffer containing 5 mM 2-mercaptoethanol and 0.1% CHAPS [3-((3-cholamidopropyl)dimethylammonio)-1-propanesulfonate], pH 7.5, to give a crude enzyme solution. This crude enzyme solution was subjected to column chromatography using Q-sepharose, GDP-hexanolamine-sepharose, (GlcNAcβ1-2Manα1-6)(GlcNAcβ1-2Manα1-3)Manβ1-4GlcNAcβ1-4GlcNAc-asparagine-sepharose and the like to collect active fractions, from which the human α1-6 fucosyltransferase of the present invention could be purified.

(2) Preparation of enzyme

The crude enzyme solution obtained in (1) above was subjected to the following purification steps. That is, the solution was applied to a Q-sepharose column equilibrated with Tris-HCl buffer containing 5 mM 2-mercaptoethanol and 0.1% CHAPS, pH 7.5. The column was washed with a 5-fold amount of the same buffer and the active fractions eluted with the same buffer containing 0.1 M NaCl were collected. The active fractions were concentrated using an ultrafiltration membrane and the buffer was changed to Tris-HCl buffer containing 5 mM 2-mercaptoethanol and 0.7% CHAPS, pH 7.5, after which the fractions were applied to GDP-hexanolamine-sepharose column equilibrated with the same buffer. The elution was performed by the linear gradient of NaCl from 0 M to 0.5 M.

The active fractions from 0.15 M to 0.3 M were collected and concentrated using an ultrafiltration membrane. After desalting, the

fractions were applied to a (GlcNAcβ1-2Manα1-6)(GlcNAcβ1-2Manα1-3)Manβ1-4GlcNAcβ1-4GlcNAc-asparagine-sepharose column equilibrated with Tris-HCl buffer containing 5 mM 2-mercaptoethanol and 0.7% CHAPS, pH 7.5. The elution was performed by the linear gradient of NaCl from 0 M to 0.5 M.

The active fractions from 0.2 M to 0.5 M were collected and concentrated using an ultrafiltration membrane. Desalting gave human α1-6 fucosyltransferase.

The thus-obtained human α1-6 fucosyltransferase fractions showed a single band at a molecular weight of about 60,000 by SDS-polyacrylamide gel electrophoresis. No other activities, such as those of transferase and glycosidase, were found and this purified enzyme was sufficiently usable as a reagent for sugar chain studies.

The optimum pH (determined by changing the pH of buffer) of the enzyme of the present invention is shown in Fig. 4. The enzyme showed high activity at around pH 7.0-7.5. In this graph, the black circle shows the case when MES buffer was used and white circle shows the case when Tris-HCl buffer was used.

The pH stability of the enzyme of the present invention was examined in the same manner. Fig. 5 shows residual activity after treating the enzyme in each buffer at each pH, 4°C for 5 hours. The enzyme was comparatively stable at about pH 4-10, and particularly stable at pH 5-9. In this graph, the black triangle shows the case when acetate buffer was used, the black circle shows the case when MES buffer was used, the white circle shows the case when Tris-HCl buffer was used, and the white triangle shows the case when sodium hydrogencarbonate buffer was used.

As shown in Fig. 6, the optimum temperature of the enzyme of the present invention was found to be at about 37°C and the enzyme was considered to retain sufficient activity in the range of 20-40°C. The frozen product was stable at -20°C for at least several months.

The enzyme showed sufficient activity in the absence of divalent metal ion. Inasmuch as it showed sufficient activity even in the

presence of 5 mM EDTA, which is a chelating agent, it is concluded that the enzyme does not require a divalent metal ion.

Example 8

Determination of amino acid sequence of human α1-6 fucosyltransferase

Purified human α1-6 fucosyltransferase (1 μg) was subjected to SDS-polyacrylamide gel electrophoresis, after which the protein was transferred to PVDF membrane (Millipore) by electroblotting. The PVDF membrane was stained with Coomassie Brilliant Blue G250, and a single band of α1-6 fucosyltransferase was detected at about 60 kDa. Then, the PVDF membrane containing said band was cut out, and, after destaining with 50% methanol, subjected to Biosystem 473A protein sequencer (Applied Biosystems) to determine amino terminal amino acid sequence of human α1-6 fucosyltransferase. The amino acid sequence determined is depicted in Sequence Listing, SEQ ID NO:11.

Example 9

Determination of partial amino acid sequence of human α1-6 fucosyltransferase

Purified human α1-6 fucosyltransferase (5 μg) was mixed with lysine endopeptidase and subjected to SDS-polyacrylamide gel electrophoresis, after which the peptide fragments were transferred to PVDF membrane (Millipore) by electroblotting. The PVDF membrane was stained with Coomassie Brilliant Blue G250, and several bands containing peptide fragments, inclusive of two main bands, were detected. Then, the PVDF membrane containing each main band was cut out and destained with 50% methanol. Said membrane was subjected to Biosystem 473A protein sequencer (Applied Biosystems) to determine the internal partial amino acid sequence of human α1-6 fucosyltransferase. The determined amino acid sequences are depicted in Sequence Listing, SEQ ID NO:12 and SEQ ID NO:13.

Example 10

Preparation of probe DNA by PCR

Mixed primers shown by SEQ ID NO:14 and SEQ ID NO:15 were synthesized from the amino acid sequences obtained in Example 9. The

mixed primer shown in SEQ ID NO:14 was used as a sense primer, and the mixed primer shown in SEQ ID NO:15 was used as an antisense primer for PCR. To be specific, 36 cycles of PCR were performed wherein PCR at 94°C (30 sec), 46°C (30 sec) and 72°C (1.5 min) using 2 μg of human-derived cDNA, 25 pmole of sense primer (mixed primer shown in SEQ ID NO: 14), 25 pmole of antisense primer (mixed primer shown in SEQ ID NO:15) and a reaction mixture (50 μl) of 50 mM potassium chloride-10 mM Tris-HCl buffer (pH 8.3)-1.5 mM magnesium chloride-0.001% gelatin-200 μM dNTP, containing 2.5 units of Taq DNA polymerase, was one cycle.

The reaction mixture (10 μl) after PCR was subjected to 2.0% agarose gel electrophoresis to confirm the PCR reaction product DNA fragments. As a result, about 200 bp DNA fragment was confirmed by agarose gel electrophoresis.

This DNA fragment was subcloned into plasmid pT7BLUEt-Vector (Novagen) and the nucleotide sequence was confirmed. As a result, the DNA fragment was found to encode the amino acid sequence depicted in Sequence Listing, SEQ ID NO:12 and SEQ ID NO:13, whereby the DNA fragment was confirmed to be a part of α1-6 fucosyltransferase gene.

Example 11

Isolation of human α1-6 fucosyltransferase gene

The DNA fragment obtained in Example 10 was labeled with [α-^{32}P]dCTP (3000 Ci/mmol, Amersham) and used as a probe to screen clones containing cDNA encoding human α1-6 fucosyltransferase, from human gastric cancer cell MKN45-derived λ ZAP cDNA library by plaque hybridization method. As a result of screening of about 2,000,000 plaques, 8 positive clones c1 to c8 were obtained. Said clones c1 to c7 were postulated to contain a full length α1-6 fucosyltransferase gene in view of the restriction enzyme cleavage site and their length. The nucleotide sequences of c1 and c2 were determined, as a result of which a nucleotide sequence depicted in SEQ ID NO:9 was obtained.

Example 12

Expression of human α1-6 fucosyltransferase

The coding region of human α1-6 fucosyltransferase gene was

subcloned into expression vector pSVK3 from clones containing cDNA encoding the human α1-6 fucosyltransferase obtained in Example 11. An expression vector containing said α1-6 fucosyltransferase gene was introduced into COS-1 cells. After 48 hours of incubation, culture cells were collected and disrupted. The enzyme activity of α1-6 fucosyltransferase in the obtained lysate was determined. As a control, the enzyme activity of α1-6 fucosyltransferase in the lysate of COS-1 cells, into which mock pSVK3 had been introduced, was determined. As a result, the control hardly showed activity, whereas COS-cells, into which the expression vector containing said α1-6 fucosyltransferase gene had been introduced, showed a high activity of 2130 nmole/h/mg protein.

Industrial Applicability

The porcine α1-6 fucosyltransferase of the present invention differs significantly from known human α1-6 fucosyltransferase in physico-chemical properties, and shows activity under optimum reaction conditions which are closer to the physiological conditions.

The α1-6 fucosyltransferase derived from human also shows physico-chemical properties markedly different from those of known human α1-6 fucosyltransferase, showing activity under optimum reaction conditions which are closer to the physiological conditions. Hence, the present invention enables development of glyco-technology inclusive of modification and synthesis of sugar chain, and of a method for diagnosis of diseases, such as cancer, which includes the use of an antibody specific for the enzyme of the present invention or the gene thereof.

Sequence Listing

Sequence No. : 1

Sequence length : 1728

Sequence type : nucleic acid

Strandedness : double

Topology : linear

Molecule type : cDNA to mRNA

Features of sequence

Original source

Organism : pig

Sequence

```
ATG CGG CCA TGG ACT GGT TCG TGG CGT TGG ATT ATG CTC ATT CTT TTT   48
Met Arg Pro Trp Thr Gly Ser Trp Arg Trp Ile Met Leu Ile Leu Phe
 1               5                  10                  15

GCC TGG GGG ACC TTG CTA TTT TAC ATA GGT GGT CAC TTG GTA CGA GAT   96
Ala Trp Gly Thr Leu Leu Phe Tyr Ile Gly Gly His Leu Val Arg Asp
            20                  25                  30

AAT GAC CAC TCT GAT CAC TCT AGC CGA GAA CTG TCC AAG ATT TTG GCA  144
Asn Asp His Ser Asp His Ser Ser Arg Glu Leu Ser Lys Ile Leu Ala
        35                  40                  45

AAG CTG GAA CGC TTA AAA CAA CAA AAT GAA GAC TTG AGG AGA ATG GCT  192
Lys Leu Glu Arg Leu Lys Gln Gln Asn Glu Asp Leu Arg Arg Met Ala
    50                  55                  60

GAA TCT CTC CGA ATA CCA GAA GGC CCC ATT GAT CAG GGG CCA GCT TCA  240
Glu Ser Leu Arg Ile Pro Glu Gly Pro Ile Asp Gln Gly Pro Ala Ser
65                  70                  75                  80

GGA AGA GTT CGT GCT TTA GAA GAG CAA TTT ATG AAG GCC AAA GAA CAG  288
Gly Arg Val Arg Ala Leu Glu Glu Gln Phe Met Lys Ala Lys Glu Gln
                85                  90                  95
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ATT GAA AAT TAT AAG AAA CAA ACT AAA AAT GGT CCA GGG AAG GAT CAT 336
Ile Glu Asn Tyr Lys Lys Gln Thr Lys Asn Gly Pro Gly Lys Asp His
100 105 110
GAA ATC CTA AGG AGG AGG ATT GAA AAT GGA GCT AAA GAG CTC TGG TTT 384
Glu Ile Leu Arg Arg Arg Ile Glu Asn Gly Ala Lys Glu Leu Trp Phe
115 120 125
TTT CTA CAA AGT GAG TTG AAG AAA TTA AAG AAT TTA GAA GGA AAT GAA 432
Phe Leu Gln Ser Glu Leu Lys Lys Leu Lys Asn Leu Glu Gly Asn Glu
130 135 140
CTC CAA AGA CAT GCA GAT GAA TTT CTA TCA GAT TTG GGA CAT CAT GAA 480
Leu Gln Arg His Ala Asp Glu Phe Leu Ser Asp Leu Gly His His Glu
145 150 155 160
AGG TCT ATA ATG ACG GAT CTA TAC TAC CTC AGT CAA ACA GAT GGG GCA 528
Arg Ser Ile Met Thr Asp Leu Tyr Tyr Leu Ser Gln Thr Asp Gly Ala
165 170 175
GGT GAT TGG CGT GAA AAG GAG GCC AAA GAT CTG ACA GAG CTG GTC CAG 576
Gly Asp Trp Arg Glu Lys Glu Ala Lys Asp Leu Thr Glu Leu Val Gln
180 185 190
CGG AGA ATA ACA TAT CTT CAG AAT CCC AAG GAC TGC AGC AAA GCC AAG 624
Arg Arg Ile Thr Tyr Leu Gln Asn Pro Lys Asp Cys Ser Lys Ala Lys
195 200 205
AAG CTA GTG TGT AAT ATC AAC AAA GGC TGT GGC TAT GGC TGT CAG CTC 672
Lys Leu Val Cys Asn Ile Asn Lys Gly Cys Gly Tyr Gly Cys Gln Leu
210 215 220
CAT CAT GTA GTG TAC TGC TTT ATG ATT GCA TAT GGC ACC CAG CGA ACA 720
His His Val Val Tyr Cys Phe Met Ile Ala Tyr Gly Thr Gln Arg Thr
225 230 235 240
CTC GCC TTG GAA TCT CAC AAT TGG CGC TAC GCT ACT GGG GGA TGG GAA 768
Leu Ala Leu Glu Ser His Asn Trp Arg Tyr Ala Thr Gly Gly Trp Glu

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                245                 250                 255
ACT GTG TTT AGA CCT GTA AGT GAG ACG TGC ACA GAC AGA TCT GGC AGC  816
Thr Val Phe Arg Pro Val Ser Glu Thr Cys Thr Asp Arg Ser Gly Ser
            260                 265                 270
TCC ACT GGA CAT TGG TCA GGT GAA GTA AAG GAC AAA AAT GTT CAG GTG  864
Ser Thr Gly His Trp Ser Gly Glu Val Lys Asp Lys Asn Val Gln Val
        275                 280                 285
GTT GAG CTC CCC ATT GTA GAC AGT GTT CAT CCT CGT CCT CCA TAT TTA  912
Val Glu Leu Pro Ile Val Asp Ser Val His Pro Arg Pro Pro Tyr Leu
    290                 295                 300
CCC CTG GCT GTC CCA GAA GAC CTT GCA GAT CGA CTT GTA CGA GTC CAT  960
Pro Leu Ala Val Pro Glu Asp Leu Ala Asp Arg Leu Val Arg Val His
305                 310                 315                 320
GGT GAT CCT GCA GTG TGG TGG GTA TCC CAG TTT GTC AAG TAC TTG ATT 1008
Gly Asp Pro Ala Val Trp Trp Val Ser Gln Phe Val Lys Tyr Leu Ile
                325                 330                 335
CGC CCA CAA CCC TGG CTG GAA AAG GAA ATA GAA GAG GCC ACC AAG AAG 1056
Arg Pro Gln Pro Trp Leu Glu Lys Glu Ile Glu Glu Ala Thr Lys Lys
            340                 345                 350
CTA GGC TTC AAA CAT CCA GTT ATT GGA GTC CAT GTT AGA CGC ACA GAC 1104
Leu Gly Phe Lys His Pro Val Ile Gly Val His Val Arg Arg Thr Asp
        355                 360                 365
AAA GTG GGA GCG GAA GCA GCC TTC CAT CCC ATT GAG GAA TAC ACG GTG 1152
Lys Val Gly Ala Glu Ala Ala Phe His Pro Ile Glu Glu Tyr Thr Val
    370                 375                 380
CAC GTT GAA GAA GAC TTT CAG CTT CTT GCT CGC AGA ATG CAA GTG GAT 1200
His Val Glu Glu Asp Phe Gln Leu Leu Ala Arg Arg Met Gln Val Asp
385                 390                 395                 400
AAA AAA AGG GTG TAT TTG GCC ACA GAT GAC CCT GCT TTG TTA AAA GAG 1248
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Lys Lys Arg Val Tyr Leu Ala Thr Asp Asp Pro Ala Leu Leu Lys Glu

405 410 415

GCA AAA ACA AAG TAC CCC AGT TAT GAA TTT ATT AGT GAT AAC TCT ATC 1296

Ala Lys Thr Lys Tyr Pro Ser Tyr Glu Phe Ile Ser Asp Asn Ser Ile

420 425 430

TCT TGG TCA GCT GGA CTA CAT AAT CGA TAT ACA GAA AAT TCA CTT CGG 1344

Ser Trp Ser Ala Gly Leu His Asn Arg Tyr Thr Glu Asn Ser Leu Arg

435 440 445

GGT GTG ATC CTG GAT ATA CAC TTT CTC TCC CAG GCA GAC TTC CTA GTG 1392

Gly Val Ile Leu Asp Ile His Phe Leu Ser Gln Ala Asp Phe Leu Val

450 455 460

TGT ACT TTT TCA TCG CAG GTC TGT AGA GTT GCT TAT GAA ATC ATG CAA 1440

Cys Thr Phe Ser Ser Gln Val Cys Arg Val Ala Tyr Glu Ile Met Gln

465 470 475 480

GCG CTG CAT CCT GAT GCC TCT GCG AAC TTC CGT TCT TTG GAT GAC ATC 1488

Ala Leu His Pro Asp Ala Ser Ala Asn Phe Arg Ser Leu Asp Asp Ile

485 490 495

TAC TAT TTT GGA GGC CCA AAT GCC CAC AAC CAA ATT GCC ATT TAT CCT 1536

Tyr Tyr Phe Gly Gly Pro Asn Ala His Asn Gln Ile Ala Ile Tyr Pro

500 505 510

CAC CAA CCT CGA ACT GAA GGA GAA ATC CCC ATG GAA CCT GGA GAT ATT 1584

His Gln Pro Arg Thr Glu Gly Glu Ile Pro Met Glu Pro Gly Asp Ile

515 520 525

ATT GGT GTG GCT GGA AAT CAC TGG GAT GGC TAT CCT AAA GGT GTT AAC 1632

Ile Gly Val Ala Gly Asn His Trp Asp Gly Tyr Pro Lys Gly Val Asn

530 535 540

AGA AAA CTG GGA AGG ACG GGC CTA TAT CCC TCC TAC AAA GTT CGA GAC 1680

Arg Lys Leu Gly Arg Thr Gly Leu Tyr Pro Ser Tyr Lys Val Arg Glu

545 550 555 560

AAG ATA GAA ACA GTC AAG TAC CCC ACA TAT CCC GAG GCT GAC AAG TAA 1728
Lys Ile Glu Thr Val Lys Tyr Pro Thr Tyr Pro Glu Ala Asp Lys
565 570 575

Sequence No. : 2
Sequence length : 575
Sequence type : amino acid
Topology : linear
Molecule type : protein
Sequence

Met Arg Pro Trp Thr Gly Ser Trp Arg Trp Ile Met Leu Ile Leu Phe
1 5 10 15
Ala Trp Gly Thr Leu Leu Phe Tyr Ile Gly Gly His Leu Val Arg Asp
20 25 30
Asn Asp His Ser Asp His Ser Ser Arg Glu Leu Ser Lys Ile Leu Ala
35 40 45
Lys Leu Glu Arg Leu Lys Gln Gln Asn Glu Asp Leu Arg Arg Met Ala
50 55 60
Glu Ser Leu Arg Ile Pro Glu Gly Pro Ile Asp Gln Gly Pro Ala Ser
65 70 75 80
Gly Arg Val Arg Ala Leu Glu Glu Gln Phe Met Lys Ala Lys Glu Gln
85 90 95
Ile Glu Asn Tyr Lys Lys Gln Thr Lys Asn Gly Pro Gly Lys Asp His
100 105 110
Glu Ile Leu Arg Arg Arg Ile Glu Asn Gly Ala Lys Glu Leu Trp Phe
115 120 125
Phe Leu Gln Ser Glu Leu Lys Lys Leu Lys Asn Leu Glu Gly Asn Glu
130 135 140
Leu Gln Arg His Ala Asp Glu Phe Leu Ser Asp Leu Gly His His Glu

145 150 155 160

Arg Ser Ile Met Thr Asp Leu Tyr Tyr Leu Ser Gln Thr Asp Gly Ala

165 170 175

Gly Asp Trp Arg Glu Lys Glu Ala Lys Asp Leu Thr Glu Leu Val Gln

180 185 190

Arg Arg Ile Thr Tyr Leu Gln Asn Pro Lys Asp Cys Ser Lys Ala Lys

195 200 205

Lys Leu Val Cys Asn Ile Asn Lys Gly Cys Gly Tyr Gly Cys Gln Leu

210 215 220

His His Val Val Tyr Cys Phe Met Ile Ala Tyr Gly Thr Gln Arg Thr

225 230 235 240

Leu Ala Leu Glu Ser His Asn Trp Arg Tyr Ala Thr Gly Gly Trp Glu

245 250 255

Thr Val Phe Arg Pro Val Ser Glu Thr Cys Thr Asp Arg Ser Gly Ser

260 265 270

Ser Thr Gly His Trp Ser Gly Glu Val Lys Asp Lys Asn Val Gln Val

275 280 285

Val Glu Leu Pro Ile Val Asp Ser Val His Pro Arg Pro Pro Tyr Leu

290 295 300

Pro Leu Ala Val Pro Glu Asp Leu Ala Asp Arg Leu Val Arg Val His

305 310 315 320

Gly Asp Pro Ala Val Trp Trp Val Ser Gln Phe Val Lys Tyr Leu Ile

325 330 335

Arg Pro Gln Pro Trp Leu Glu Lys Glu Ile Glu Glu Ala Thr Lys Lys

340 345 350

Leu Gly Phe Lys His Pro Val Ile Gly Val His Val Arg Arg Thr Asp

355 360 365

Lys Val Gly Ala Glu Ala Ala Phe His Pro Ile Glu Glu Tyr Thr Val

370 375 380

His Val Glu Glu Asp Phe Gln Leu Leu Ala Arg Arg Met Gln Val Asp
385 390 395 400
Lys Lys Arg Val Tyr Leu Ala Thr Asp Asp Pro Ala Leu Leu Lys Glu
405 410 415
Ala Lys Thr Lys Tyr Pro Ser Tyr Glu Phe Ile Ser Asp Asn Ser Ile
420 425 430
Ser Trp Ser Ala Gly Leu His Asn Arg Tyr Thr Glu Asn Ser Leu Arg
435 440 445
Gly Val Ile Leu Asp Ile His Phe Leu Ser Gln Ala Asp Phe Leu Val
450 455 460
Cys Thr Phe Ser Ser Gln Val Cys Arg Val Ala Tyr Glu Ile Met Gln
465 470 475 480
Ala Leu His Pro Asp Ala Ser Ala Asn Phe Arg Ser Leu Asp Asp Ile
485 490 495
Tyr Tyr Phe Gly Gly Pro Asn Ala His Asn Gln Ile Ala Ile Tyr Pro
500 505 510
His Gln Pro Arg Thr Glu Gly Glu Ile Pro Met Glu Pro Gly Asp Ile
515 520 525
Ile Gly Val Ala Gly Asn His Trp Asp Gly Tyr Pro Lys Gly Val Asn
530 535 540
Arg Lys Leu Gly Arg Thr Gly Leu Tyr Pro Ser Tyr Lys Val Arg Glu
545 550 555 560
Lys Ile Glu Thr Val Lys Tyr Pro Thr Tyr Pro Glu Ala Asp Lys
565 570 575

Sequence No. : 3
Sequence length : 26
Sequence type : amino acid
Topology : linear

Molecule type : peptide

Sequence

Lys Gln Thr Lys Asn Gly Pro Gly Lys Asp His Glu Ile Leu Arg Arg

5 10 15

Arg Ile Glu Asn Gly Ala Lys Glu Leu Gln

20 25

Sequence No. : 4

Sequence length : 10

Sequence type : amino acid

Topology : linear

Molecule type : peptide

Sequence

Lys Tyr Pro Thr Tyr Pro Glu Ala Asp Lys

5 10

Sequence No. : 5

Sequence length : 12

Sequence type : amino acid

Topology : linear

Molecule type : peptide

Sequence

Lys Tyr Leu Ile Arg Pro Gln Pro Trp Leu Glu Lys

5 10

Sequence No. : 6

Sequence length : 14

Sequence type : amino acid

Topology : linear

Molecule type : peptide

Sequence

Lys Arg Val Tyr Leu Ala Thr Asp Asp Pro Ala Leu Leu Lys

5 10

Sequence No. : 7

Sequence length : 19

Sequence type : nucleic acid

Strandedness : single

Topology : linear

Molecule type : DNA

Sequence

AARSAR ACNAA RAAYG GNCC 19

Sequence No. : 8

Sequence length : 20

Sequence type : nucleic acid

Strandedness : single

Topology : linear

Molecule type : DNA

Sequence

TCNGG RTANG TNGGR TAYTT 20

Sequence No. : 9

Sequence length : 2100

Sequence type : nucleic acid

Strandedness : double

Topology : linear

Molecule type : cDNA to mRNA

Features of sequence

Original source

Organism : human

Sequence

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                                                    AAGCTTC CTACACATAT   17
CACCAGGAGG ATCTCTTTGA AAGATTCACT GCAGGACTAC CAGAGAGAAT AATTTGTCTG   77
AAGCATCATG TGTTGAAACA ACAGAAGTCT ATTCACCTGT GCACTAACTA GAAACAGAGT  137
TACAATGTTT TCAATTCTTT GAGCTCCAGG ACTCCAGGGA AGTGAGTTGA AAATCTGAAA  197
ATG CGG CCA TGG ACT GGT TCC TGG CGT TGG ATT ATG CTC ATT CTT TTT     245
Met Arg Pro Trp Thr Gly Ser Trp Arg Trp Ile Met Leu Ile Leu Phe
                5                  10                  15
GCC TGG GGG ACC TTG CTG TTT TAT ATA GGT GGT CAC TTG GTA CGA GAT     293
Ala Trp Gly Thr Leu Leu Phe Tyr Ile Gly Gly His Leu Val Arg Asp
            20                  25                  30
AAT GAC CAT CCT GAT CAC TCT AGC CGA GAA CTG TCC AAG ATT CTG GCA     341
Asn Asp His Pro Asp His Ser Ser Arg Glu Leu Ser Lys Ile Leu Ala
        35                  40                  45
AAG CTT GAA CGC TTA AAA CAG CAG AAT GAA GAC TTG AGG CGA ATG GCC     389
Lys Leu Glu Arg Leu Lys Gln Gln Asn Glu Asp Leu Arg Arg Met Ala
    50                  55                  60
GAA TCT CTC CGG ATA CCA GAA GGC CCT ATT GAT CAG GGG CCA GCT ATA     437
Glu Ser Leu Arg Ile Pro Glu Gly Pro Ile Asp Gln Gly Pro Ala Ile
65                  70                  75                  80
GGA AGA GTA CGC GTT TTA GAA GAG CAG CTT GTT AAG GCC AAA GAA CAG     485
Gly Arg Val Arg Val Leu Glu Glu Gln Leu Val Lys Ala Lys Glu Gln
                85                  90                  95
ATT GAA AAT TAC AAG AAA CAG ACC AGA AAT GGT CTG GGG AAG GAT CAT     533
Ile Glu Asn Tyr Lys Lys Gln Thr Arg Asn Gly Leu Gly Lys Asp His
            100                 105                 110
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GAA ATC CTG AGG AGG AGG ATT GAA AAT GGA GCT AAA GAG CTC TGG TTT 581
Glu Ile Leu Arg Arg Arg Ile Glu Asn Gly Ala Lys Glu Leu Trp Phe
115 120 125
TTC CTA CAG AGT GAA TTG AAG AAA TTA AAG AAC TTA GAA GGA AAT GAA 629
Phe Leu Gln Ser Glu Leu Lys Lys Leu Lys Asn Leu Glu Gly Asn Glu
130 135 140
CTC CAA AGA CAT GCA GAT GAA TTT CTT TTG GAT TTA GGA CAT CAT GAA 677
Leu Gln Arg His Ala Asp Glu Phe Leu Leu Asp Leu Gly His His Glu
145 150 155 160
AGG TCT ATA ATG ACG GAT CTA TAC TAC CTC AGT CAG ACA GAT GGA GCA 725
Arg Ser Ile Met Thr Asp Leu Tyr Tyr Leu Ser Gln Thr Asp Gly Ala
165 170 175
GGT GAT TGG CGG GAA AAA GAG GCC AAA GAT CTG ACA GAA CTG GTT CAG 773
Gly Asp Trp Arg Glu Lys Glu Ala Lys Asp Leu Thr Glu Leu Val Gln
180 185 190
CGG AGA ATA ACA TAT CTT CAG AAT CCC AAG GAC TGC AGC AAA GCC AAA 821
Arg Arg Ile Thr Tyr Leu Gln Asn Pro Lys Asp Cys Ser Lys Ala Lys
195 200 205
AAG CTG GTG TGT AAT ATC AAC AAA GGC TGT GGC TAT GGC TGT CAG CTC 869
Lys Leu Val Cys Asn Ile Asn Lys Gly Cys Gly Tyr Gly Cys Gln Leu
210 215 220
CAT CAT GTG GTC TAC TGC TTC ATG ATT GCA TAT GGC ACC CAG CGA ACA 917
His His Val Val Tyr Cys Phe Met Ile Ala Tyr Gly Thr Gln Arg Thr
225 230 235 240
CTC ATC TTG GAA TCT CAG AAT TGG CGC TAT GCT ACT GGT GGA TGG GAG 965
Leu Ile Leu Glu Ser Gln Asn Trp Arg Tyr Ala Thr Gly Gly Trp Glu
245 250 255
ACT GTA TTT AGG CCT GTA AGT GAG ACA TGC ACA GAC AGA TCT GGC ATC 1013
Thr Val Phe Arg Pro Val Ser Glu Thr Cys Thr Asp Arg Ser Gly Ile

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                260                 265                 270
TCC ACT GGA CAC TGG TCA GGT GAA GTG AAG GAC AAA AAT GTT CAA GTG   1061
Ser Thr Gly His Trp Ser Gly Glu Val Lys Asp Lys Asn Val Gln Val
        275                 280                 285
GTC GAG CTT CCC ATT GTA GAC AGT CTT CAT CCC CGT CCT CCA TAT TTA   1109
Val Glu Leu Pro Ile Val Asp Ser Leu His Pro Arg Pro Pro Tyr Leu
    290                 295                 300
CCC TTG GCT GTA CCA GAA GAC CTC GCA GAT CGA CTT GTA CGA GTG CAT   1157
Pro Leu Ala Val Pro Glu Asp Leu Ala Asp Arg Leu Val Arg Val His
305                 310                 315                 320
GGT GAC CCT GCA GTG TGG TGG GTG TCT CAG TTT GTC AAA TAC TTG ATC   1205
Gly Asp Pro Ala Val Trp Trp Val Ser Gln Phe Val Lys Tyr Leu Ile
                325                 330                 335
CGC CCA CAG CCT TGG CTA GAA AAA GAA ATA GAA GAA GCC ACC AAG AAG   1253
Arg Pro Gln Pro Trp Leu Glu Lys Glu Ile Glu Glu Ala Thr Lys Lys
            340                 345                 350
CTT GGC TTC AAA CAT CCA GTT ATT GGA GTC CAT GTC AGA CGC ACA GAC   1301
Leu Gly Phe Lys His Pro Val Ile Gly Val His Val Arg Arg Thr Asp
        355                 360                 365
AAA GTG GGA ACA GAA GCT GCC TTC CAT CCC ATT GAA GAG TAC ATG GTG   1349
Lys Val Gly Thr Glu Ala Ala Phe His Pro Ile Glu Glu Tyr Met Val
    370                 375                 380
CAT GTT GAA GAA CAT TTT CAG CTT CTT GCA CGC AGA ATG CAA GTG GAC   1397
His Val Glu Glu His Phe Gln Leu Leu Ala Arg Arg Met Gln Val Asp
385                 390                 395                 400
AAA AAA AGA GTG TAT TTG GCC ACA GAT GAC CCT TCT TTA TTA AAG GAG   1445
Lys Lys Arg Val Tyr Leu Ala Thr Asp Asp Pro Ser Leu Leu Lys Glu
                405                 410                 415
GCA AAA ACA AAG TAC CCC AAT TAT GAA TTT ATT AGT GAT AAC TCT ATT   1493
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Ala Lys Thr Lys Tyr Pro Asn Tyr Glu Phe Ile Ser Asp Asn Ser Ile

420 425 430

TCC TGG TCA GCT GGA CTG CAC AAT CGA TAC ACA GAA AAT TCA CTT CGT 1541

Ser Trp Ser Ala Gly Leu His Asn Arg Tyr Thr Glu Asn Ser Leu Arg

435 440 445

GGA GTG ATC CTG GAT ATA CAT TTT CTC TCT CAG GCA GAC TTC CTA GTG 1589

Gly Val Ile Leu Asp Ile His Phe Leu Ser Gln Ala Asp Phe Leu Val

450 455 460

TGT ACT TTT TCA TCC CAG GTC TGT CGA GTT GCT TAT GAA ATT ATG CAA 1637

Cys Thr Phe Ser Ser Gln Val Cys Arg Val Ala Tyr Glu Ile Met Gln

465 470 475 480

ACA CTA CAT CCT GAT GCC TCT GCA AAC TTC CAT TCT TTA GAT GAC ATC 1685

Thr Leu His Pro Asp Ala Ser Ala Asn Phe His Ser Leu Asp Asp Ile

485 490 495

TAC TAT TTT GGG GGC CAG AAT GCC CAC AAT CAA ATT GCC ATT TAT GCT 1733

Tyr Tyr Phe Gly Gly Gln Asn Ala His Asn Gln Ile Ala Ile Tyr Ala

500 505 510

CAC CAA CCC CGA ACT GCA GAT GAA ATT CCC ATG GAA CCT GGA GAT ATC 1781

His Gln Pro Arg Thr Ala Asp Glu Ile Pro Met Glu Pro Gly Asp Ile

515 520 525

ATT GGT GTG GCT GGA AAT CAT TGG GAT GGC TAT TCT AAA GGT GTC AAC 1829

Ile Gly Val Ala Gly Asn His Trp Asp Gly Tyr Ser Lys Gly Val Asn

530 535 540

AGG AAA TTG GGA AGG ACG GGC CTA TAT CCC TCC TAC AAA GTT CGA GAG 1877

Arg Lys Leu Gly Arg Thr Gly Leu Tyr Pro Ser Tyr Lys Val Arg Glu

545 550 555 560

AAG ATA GAA ACG GTC AAG TAC CCC ACA TAT CCT GAG GCT GAG AAA TAA 1925

Lys Ile Glu Thr Val Lys Tyr Pro Thr Tyr Pro Glu Ala Glu Lys

565 570 575

AGCTCAGATG GAAGAGATAA ACGACCAAAC TCAGTTCGAC CAAACTCAGT TCAAACCATT 1985

TCAGCCAAAC TGTAGATGAA GAGGGCTCTG ATCTAACAAA ATAAGGTTAT ATGAGTAGAT 2045

ACTCTCAGCA CCAAGAGCAG CTGGGAACTG ACATAGGCTT CAATTGGTGG AATTC 2100

Sequence No. : 10

Sequence length : 575

Sequence type : amino acid

Topology : linear

Molecule type : protein

Sequence

Met Arg Pro Trp Thr Gly Ser Trp Arg Trp Ile Met Leu Ile Leu Phe
1 5 10 15

Ala Trp Gly Thr Leu Leu Phe Tyr Ile Gly Gly His Leu Val Arg Asp
20 25 30

Asn Asp His Pro Asp His Ser Ser Arg Glu Leu Ser Lys Ile Leu Ala
35 40 45

Lys Leu Glu Arg Leu Lys Gln Gln Asn Glu Asp Leu Arg Arg Met Ala
50 55 60

Glu Ser Leu Arg Ile Pro Glu Gly Pro Ile Asp Gln Gly Pro Ala Ile
65 70 75 80

Gly Arg Val Arg Val Leu Glu Glu Gln Leu Val Lys Ala Lys Glu Gln
85 90 95

Ile Glu Asn Tyr Lys Lys Gln Thr Arg Asn Gly Leu Gly Lys Asp His
100 105 110

Glu Ile Leu Arg Arg Arg Ile Glu Asn Gly Ala Lys Glu Leu Trp Phe
115 120 125

Phe Leu Gln Ser Glu Leu Lys Lys Leu Lys Asn Leu Glu Gly Asn Glu
130 135 140

Leu Gln Arg His Ala Asp Glu Phe Leu Leu Asp Leu Gly His His Glu

145 150 155 160

Arg Ser Ile Met Thr Asp Leu Tyr Tyr Leu Ser Gln Thr Asp Gly Ala

165 170 175

Gly Asp Trp Arg Glu Lys Glu Ala Lys Asp Leu Thr Glu Leu Val Gln

180 185 190

Arg Arg Ile Thr Tyr Leu Gln Asn Pro Lys Asp Cys Ser Lys Ala Lys

195 200 205

Lys Leu Val Cys Asn Ile Asn Lys Gly Cys Gly Tyr Gly Cys Gln Leu

210 215 220

His His Val Val Tyr Cys Phe Met Ile Ala Tyr Gly Thr Gln Arg Thr

225 230 235 240

Leu Ile Leu Glu Ser Gln Asn Trp Arg Tyr Ala Thr Gly Gly Trp Glu

245 250 255

Thr Val Phe Arg Pro Val Ser Glu Thr Cys Thr Asp Arg Ser Gly Ile

260 265 270

Ser Thr Gly His Trp Ser Gly Glu Val Lys Asp Lys Asn Val Gln Val

275 280 285

Val Glu Leu Pro Ile Val Asp Ser Leu His Pro Arg Pro Pro Tyr Leu

290 295 300

Pro Leu Ala Val Pro Glu Asp Leu Ala Asp Arg Leu Val Arg Val His

305 310 315 320

Gly Asp Pro Ala Val Trp Trp Val Ser Gln Phe Val Lys Tyr Leu Ile

325 330 335

Arg Pro Gln Pro Trp Leu Glu Lys Glu Ile Glu Glu Ala Thr Lys Lys

340 345 350

Leu Gly Phe Lys His Pro Val Ile Gly Val His Val Arg Arg Thr Asp

355 360 365

Lys Val Gly Thr Glu Ala Ala Phe His Pro Ile Glu Glu Tyr Met Val

370 375 380

His Val Glu Glu His Phe Gln Leu Leu Ala Arg Arg Met Gln Val Asp
385 390 395 400
Lys Lys Arg Val Tyr Leu Ala Thr Asp Asp Pro Ser Leu Leu Lys Glu
405 410 415
Ala Lys Thr Lys Tyr Pro Asn Tyr Glu Phe Ile Ser Asp Asn Ser Ile
420 425 430
Ser Trp Ser Ala Gly Leu His Asn Arg Tyr Thr Glu Asn Ser Leu Arg
435 440 445
Gly Val Ile Leu Asp Ile His Phe Leu Ser Gln Ala Asp Phe Leu Val
450 455 460
Cys Thr Phe Ser Ser Gln Val Cys Arg Val Ala Tyr Glu Ile Met Gln
465 470 475 480
Thr Leu His Pro Asp Ala Ser Ala Asn Phe His Ser Leu Asp Asp Ile
485 490 495
Tyr Tyr Phe Gly Gly Gln Asn Ala His Asn Gln Ile Ala Ile Tyr Ala
500 505 510
His Gln Pro Arg Thr Ala Asp Glu Ile Pro Met Glu Pro Gly Asp Ile
515 520 525
Ile Gly Val Ala Gly Asn His Trp Asp Gly Tyr Ser Lys Gly Val Asn
530 535 540
Arg Lys Leu Gly Arg Thr Gly Leu Tyr Pro Ser Tyr Lys Val Arg Glu
545 550 555 560
Lys Ile Glu Thr Val Lys Tyr Pro Thr Tyr Pro Glu Ala Glu Lys ---
565 570 575

Sequence No. : 11
Sequence length : 14
Sequence type : amino acid
Topology : linear

Molecule type : peptide

Sequence

Arg Ile Pro Glu Gly Pro Ile Asp Gln Gly Pro Ala Ile Gly

5 10

Sequence No. : 12

Sequence length : 25

Sequence type : amino acid

Topology : linear

Molecule type : peptide

Sequence

Lys Leu Gly Phe Lys His Pro Val Ile Gly Val His Val Arg Arg Thr

5 10 15

Asp Lys Val Gly Thr Glu Ala Ala Phe

20 25

Sequence No. : 13

Sequence length : 13

Sequence type : amino acid

Topology : linear

Molecule type : peptide

Sequence

Thr Lys Tyr Pro Asn Tyr Glu Phe Ile Ser Asp Asn Ser

5 10

Sequence No. : 14

Sequence length : 20

Sequence type : nucleic acid

Strandedness : single

Topology : linear

Molecule type : DNA

Sequence

TTYAA RCAYC CHGTB ATYGG 20

Sequence No. : 15

Sequence length : 20

Sequence type : nucleic acid

Strandedness : single

Topology : linear

Molecule type : DNA

Sequence

GWRTT RTCRG WRATR AAYTC 20